System and method for predicting
chromosomal regions that control phenotypic traits

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Abstract

A method of associating a phenotype with one or more candidate chromosomal regions in a genome of an organism includes the step of deriving a phenotypic data structure that represents differences in phenotypes between different strains of the organism. Further, a genotypic data structure is established. The genotypic data structure corresponds to a locus selected from a plurality of loci in the genome of the organism. The genotypic data structure represents variations of at least one component of the locus between different strains of the organism. The phenotypic data structure is compared to the genotypic data structure to form a correlation value. The process of establishing a genotypic data structure and comparing it to the phenotypic data structure is repeated for each locus in the plurality of loci, thereby identifying one or more genotypic data structures that form a high correlation value relative to all other compared genotypic data structures. The loci that correspond to the one or more genotypic data structures having a high correlation value represent the one or more candidate chromosomal regions.

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